(b) an amino acid sequence selected from the group consisting of SEQ ID NOS. 2, 4, 6, 8 and 10, wherein the amino acid sequence has at least one conservative substitution; wherein the polypeptide comprising the amino acid sequence (b) can self-assemble to form a polymer; and

(c) an amino acid sequence comprising a fragment of at least one amino acid residue of SEQ ID NOS. 2, 4, 6, 8 and 10, wherein the polypeptide comprising the amino acid sequence (c) can self-assemble to form a polymer.

4. (Amended) The drug delivery system as claimed in claim 1, wherein each of the plurality of polypeptides comprises an amino acid sequence that has at least 50% identity to an amino acid sequence selected from the group consisting of SEQ ID NOS. 2, 4, 6, 8 and 10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

5. (Amended) The drug delivery system as claimed in claim 1, wherein each of the plurality of polypeptides comprises an amino acid sequence that has at least 60% identity to an amino acid sequence selected from the group consisting of SEQ ID NOS. 2, 4, 6, 8 and 10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

6. (Amended) The drug delivery system as claimed in claim 1, wherein each of the plurality of polypeptides comprises an amino acid sequence that has at least 70% identity to an amino acid sequence selected from the group consisting of SEQ ID NOS. 2, 4, 6, 8 and 10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

7. (Amended) The drug delivery system as claimed in claim 1, wherein each of the plurality of polypeptides comprises an amino acid sequence that has at least 80% identity toan amino acid sequence selected from the group consisting of SEQ ID NOS. 2, 4, 6, 8

and10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

8. (Amended) The drug delivery system as claimed in claim 1, wherein each of the plurality of polypeptides comprises an amino acid sequence that has at least 90% identity to an amino acid sequence selected from the group consisting of SEQ ID NOS. 2, 4, 6, 8 and 10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

9. (Amended) The drug delivery system as claimed in claim 3, wherein each of the plurality of polypeptides comprises an amino acid sequence that has at least 10 consecutive amino acids of an amino acid sequence selected from the group consisting of SEQ ID NOS. 2, 4, 6, 8, and 10.

10. (Amended) The drug delivery system as claimed in claim 9, wherein each of the plurality of polypeptides comprises an amino acid sequence that has at least 50% identity to an amino acid sequence selected from the group consisting of SEQ ID NOS. 2, 4, 6, 8 and 10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

11. (Amended) The drug delivery system as claimed in claim 9, wherein each of the plurality of polypeptides comprises an amino acid sequence that has at least 60% identity to an amino acid sequence selected from the group consisting of SEQ ID NOS. 2, 4, 6, 8 and 10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

12. (Amended) The drug delivery system as claimed in claim 9, wherein each of the plurality of polypeptides comprises an amino acid sequence that has at least 70% identity to an amino acid sequence selected from the group consisting of SEQ ID NOS. 2, 4, 6, 8 and 10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

13. (Amended) The drug delivery system as claimed in claim 9, wherein each of the plurality of polypeptides comprises an amino acid sequence that has at least 80% identity to an amino acid sequence selected from the group consisting of SEQ ID NOS. 2, 4, 6, 8 and 10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

14. (Amended) The drug delivery system as claimed in claim 9, wherein each of the plurality of polypeptides comprises an amino acid sequence that has at least 90% identity to an amino acid sequence selected from the group consisting of SEQ ID NOS. 2, 4, 6, 8 and 10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

15. (Amended)The drug delivery system as claimed in claim 1, wherein each of the plurality of polypeptides is encoded by a nucleic acid molecule selected from the group consisting of:

(a) a nucleic acid molecule comprising a sequence having at least 50% homology with the nucleic acid sequence of at least one of SEQ ID NOS. 1, 3, 5, 7 and 9 over a subsequence of at least 100 residues;

(b) a nucleic acid molecule which hybridizes under low, moderate or high stringency conditions with at least one of (i) the nucleic acid sequences of SEQ ID NOS. 1, 3, 5, 7 and 9, (ii) a complementary strand of a nucleic acid sequence of at least one of SEQ ID NOS. 1, 3, 5, 7 and 9, and a subsequence thereof of at least 100 nucleotides;

(c) a subsequence of (a) or (b), wherein the subsequence encodes a polypeptide, which can self-assemble to form a polymer; and

(d) a nucleic acid molecule that encodes a polypeptide having an amino acid sequence that has at least 50% identity with at least one amino acid sequence of SEQ ID NOS. 1, 3, 5, 7 and 9, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection.

16. (Amended) The drug delivery system as claimed in claim 15, wherein each of the plurality of polypeptides is encoded by a first nucleic acid molecule, which hybridizes to a second nucleic acid molecule that has a complement of a nucleic acid sequence as set forth in SEQ ID NOS. 1, 3, 5, 7 and 9, under conditions of high stringency, wherein the conditions of high stringency are hybridization at 65°C in a hybridization buffer which comprises 3.5 times 0.15 M sodium chloride/0.015 M sodium citrate at pH 7; 0.02% Ficoll; 0.02% polyvinyl pyrrolidone; 0.02% Bovine Serum Albumin; 25 mM NaH_2PO_4 at pH 7; 0.5% sodium dodecyl sulphate; and 2 mM ethylenediaminetetracetic acid.

17. (Amended) The drug delivery system as claimed in claim 15, wherein each of the plurality of polypeptides is encoded by a first nucleic acid molecule, which hybridizes to a second nucleic acid molecule that has a complement of a nucleic acid sequence as set forth in SEQ ID NOS. 1, 3, 5, 7 and 9, under conditions of moderate stringency.

18. (Amended) The drug delivery system as claimed in claim 15, wherein each of the plurality of polypeptides is encoded by a first nucleic acid molecule, which hybridizes to a second nucleic acid molecule that has a complement of a nucleic acid sequence as set forth in SEQ ID NOS. 1, 3, 5, 7 and 9, under conditions of low stringency, wherein the low stringency conditions are prehybridization and hybridization at 42 degrees C in 5 times SSPE; 0.3% sodium dodecyl sulphate; 200 μg/ml sheared and denatured salmon sperm DNA; and 25% formamide; and washing with 2 times 0.15 M sodium chloride/0.015 M sodium citrate at pH 7, and 0.2% sodium dodecyl sulphate at 50 degrees C.

19. (Amended) The drug delivery system as claimed in claim 15, wherein said nucleic acid molecule has at least about 50% homology to at least one of SEQ ID NOS: 1, 3, 5, 7 and 9 over a subsequence of at least about 200 residues.

20. (Amended) The drug delivery system as claimed in claim 15, wherein the nucleic acid molecule comprises a sequence having at least 50% homology to at least one of SEQ ID NOS: 1, 3, 5, 7 and 9 over the entire sequence.

21. (Amended) The drug delivery system as claimed in claim 15, wherein the nucleic acid molecule comprises a sequence having at least 60% homology to at least one of SEQ ID NOS: 1, 3, 5, 7 and 9.

22. (Amended) The drug delivery system as claimed in claim 15, wherein the nucleic acid molecule comprises a sequence having at least 70% homology to at least one of SEQ ID NOS: 1, 3, 5, 7 and 9.

23. (Amended) The drug delivery system as claimed in claim 15, wherein the nucleic acid molecule comprises a sequence having at least 80% homology to at least one of SEQ ID NOS: 1, 3, 5, 7 and 9.

24. (Amended) The drug delivery system as claimed in claim 15, wherein the nucleic acid molecule comprises a sequence having at least 90% homology to at least one of SEQ ID NOS: 1, 3, 5, 7 and 9.

25. (Amended) The drug delivery system as claimed in claim 15, wherein the nucleic acid molecule comprises a sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9.

26. (Amended) The drug delivery system as claimed in claim 15, wherein the nucleic acid molecule comprises at least 10 consecutive bases of a sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9.

27. (Amended) The drug delivery system as claimed in claim 26, wherein the nucleic acid molecule comprises a sequence having at least 60% homology to a sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9.

28. (Amended) The drug delivery system as claimed in claim 26, wherein the nucleic acid molecule comprises a sequence having at least 70% homology to a sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9.

29. (Amended) The drug delivery system as claimed in claim 26, wherein the nucleic acid molecule comprises a sequence having at least 80% homology to a sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9.

30. (Amended) The drug delivery system as claimed in claim 26, wherein the nucleic acid molecule comprises a sequence having at least 90% homology to a sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9.

32. (Amended) A method as claimed in claim 31, wherein the polypeptide has an amino acid sequence selected from the group consisting of:

(a) an amino acid sequence selected from SEQ ID NOS. 2, 4, 6, 8 and10;

(b) an amino acid sequence selected from the group consisting of SEQ ID NOS. 2, 4, 6, 8 and 10, wherein the amino acid sequence has at least one conservative substitution; wherein the polypeptide comprising the amino acid sequence (b) can self-assemble to form a polymer; and

(c) an amino acid sequence comprising a fragment of at least one amino acid residue of SEQ ID NOS. 2, 4, 6, 8 and 10, wherein the polypeptide comprising the amino acid sequence (c) can self-assemble to form a polymer .

33. (Amended) A method as claimed in claim 31, wherein the polypeptide is encoded by a nucleic acid molecule selected from the group consisting of:

(a) a nucleic acid molecule comprising a sequence having at least 50% homology with the nucleic acid sequence of at least one of SEQ ID NOS. 1, 3, 5, 7 and 9, over a subsequence of at least 100 residues;

(b) a nucleic acid molecule which hybridizes under low, moderate or high stringency conditions with at least one of (i) the nucleic acid sequences of SEQ ID NOS.

1, 3, 5, 7 and 9, (ii) a complementary strand of a nucleic acid sequence of at least one of SEQ ID NOS. 1, 3, 5, 7 and 9, and a subsequence thereof of at least 100 nucleotides;

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(c) a subsequence of (a) or (b), wherein the subsequence encodes a polypeptide, which can self-assemble to form a polymer; and

(d) a nucleic acid molecule that encodes a polypeptide having an amino acid sequence that has at least 50% identity with at least one amino acid sequence of SEQ ID NOS. 1, 3, 5, 7 and 9, as determined by analysis with a sequence comparison algorithm or by visual inspection.

41. (Amended) A method of encapsulating a molecule comprising the steps of:

providing a solution of a plurality of polypeptides having an amino acid sequence selected from the group consisting of:

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(a) an amino acid sequence selected from SEQ ID NOS:. 2, 4, 6, 8 and10;

(b) an amino acid sequence selected from the group consisting of SEQ ID NOS. 2, 4, 6, 8 and 10, wherein the amino acid sequence has at least one conservative substitution; wherein the polypeptide comprising the amino acid sequence (b) can self-assemble to form a polymer; and

(c) an amino acid sequence comprising a fragment of at least one amino acid residue of SEQ ID NOS. 2, 4, 6, 8 and 10, wherein the polypeptide comprising the amino acid sequence (c) can self-assemble to form a polymer; and

polymerizing the plurality of polypeptides the presence of the molecule so as to encapsulate the molecule in the polymer.

43. (Amended) A method of encapsulating a molecule comprising the steps of:

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providing a solution of a plurality of polypeptides, wherein each polypeptide is encoded by a nucleic acid molecule selected from the group consisting of:

(a) a nucleic acid molecule comprising a sequence having at least 50% homology with the nucleic acid sequence of at least one of SEQ ID NOS. 1, 3, 5, 7 and 9 over a subsequence of at least 100 residues;

(b) a nucleic acid molecule which hybridizes under low, moderate or high stringency conditions with at least one of (i) the nucleic acid sequences of SEQ ID NOS. 1, 3, 5, 7 and 9, (ii) a complementary strand of a nucleic acid sequence of at least one of SEQ ID NOS. 1, 3, 5, 7 and 9, and a subsequence thereof of at least 100 nucleotides;

A4 (c) a subsequence of (a) or (b), wherein the subsequence encodes a polypeptide, which can self-assemble to form a polymer; and

(d) a nucleic acid molecule that encodes a polypeptide having an amino acid sequence that has at least 50% identity with at least one amino acid sequence of SEQ ID NOS. 1, 3, 5, 7 and 9, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; and

polymerizing the plurality of polypeptides the presence of the molecule so as to encapsulate the molecule in the polymer.

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45. (Amended) A method of generating a variant comprising:

obtaining a nucleic acid molecule selected from the group consisting of:

(a) a nucleic acid molecule comprising a sequence having at least 50% homology with the nucleic acid sequence of at least one of SEQ ID NOS. 1, 3, 5, 7 and 9 over a subsequence of at least 100 residues;

A5 (b) a nucleic acid molecule which hybridizes under low, moderate or high stringency conditions with at least one of (i) the nucleic acid sequences of SEQ ID NOS. 1, 3, 5, 7 and 9, (ii) a complementary strand of a nucleic acid sequence of at least one of SEQ ID NOS. 1, 3, 5, 7 and 9, and a subsequence thereof of at least 100 nucleotides;

(c) a subsequence of (a) or (b), wherein the subsequence encodes a polypeptide, which can self-assemble to form a polymer; and

(d) a nucleic acid molecule that encodes a polypeptide having an amino acid sequence that has at least 50% identity with at least one amino acid sequence of SEQ ID NOS. 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; and

modifying said sequence by one or more steps selected from the group consisting of modifying one or more nucleotides in said sequence to another nucleotide, deleting

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one or more nucleotides in said sequence, and adding one or more nucleotides to said sequence.

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60. An assay for identifying functional polypeptide fragments or variants which can self-assemble to form a polymer and are encoded by nucleic acid molecules comprising a sequence selected from the group consisting of SEQ ID NOS. 1, 3, 5, 7 and 9, a subsequence of SEQ ID NOS: 1, 3, 5, 7 and 9, and a sequence having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, , said assay comprising the steps of:

providing a solution of a plurality of polypeptides encoded by nucleic acid molecules comprising a sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9, a subsequence of SEQ ID NOS. 1, 3, 5, 7 and 9, and sequences having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, , in a solution containing a template molecule and alkaline earth metal ion; and

detecting a presence of a polymer in the solution.

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62. A polypeptide comprising:

a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10, sequences having at least 50% homology to a sequence selected from SEQ ID NOS: 2, 4, 6, 8, and 10, as determined by analysis with a sequence comparison algorithm or by visual inspection; and

at least one functional group selected from the group consisting of an antibody, an oligosaccharide, a polynucleotide, and a polyethylene glycol.

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67. A polypeptide comprising:

an amino acid sequence encoded by a sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9, variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by

analysis with a sequence comparison algorithm or by visual inspection, sequences complementary to SEQ ID NOS: 1, 3, 5, 7 and 9, and sequences complementary to variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, and isolated nucleic acids that hybridize to nucleic acids having any of the foregoing sequences under conditions of low, moderate and high stringency., and

at least one functional group selected from the group consisting of an antibody, an oligosaccharide, a polynucleotide, and a polyethylene glycol.

85. (Amended) A separation agent comprising a polymer made by self-assembly of a plurality of polypeptides each of which has at least 50% homology to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

86. (Amended) The separation agent as claimed in claim 85, wherein each of the plurality of polypeptides each of which has at least 60% homology to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

87. (Amended) The separation agent as claimed in claim 85, wherein each of the plurality of polypeptides each of which has at least 70% homology to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

88. (Amended) The separation agent as claimed in claim 85, wherein each of the plurality of polypeptides each of which has at least 80% homology to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

89. (Amended) The separation agent as claimed in claim 85, wherein each of the plurality of polypeptides each of which has at least 90% homology to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

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90. (Amended) The separation agent as claimed in claim 85, wherein each of the plurality of polypeptides is a polypeptide each of which has an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

93. (Amended) The fiber as claimed in claim 92, wherein each of the plurality of polypeptides has at least 50% homology to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

94. (Amended) A lubricant comprising:

a polymer made by self-assembly of a plurality of polypeptides, wherein each of the plurality of polypeptides has at least 50% homology to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

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95. (Amended) A coating composition comprising a polymer made by self-assembly of a plurality of polypeptides, wherein each of the plurality of polypeptides has at least 50% homology to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

96. (Amended) A biochip comprising a polymer made by self-assembly of a plurality of polypeptides, wherein each of the plurality of polypeptides has at least 50% homology to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

97. (Amended) A nanomechanical component comprising a polymer made by self-assembly of a plurality of polypeptides, wherein each of the plurality of polypeptides has

at least 50% homology to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

98. (Amended) An optical switch comprising a polymer made by self-assembly of a plurality of polypeptides, wherein each of the plurality of polypeptides has at least 60% homology to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

99. (Amended) An optical waveguide comprising a polymer made by self-assembly of a plurality of polypeptides, wherein each of the plurality of polypeptides has at least 50% homology to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

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100. (Amended) A computer readable medium having stored thereon a sequence of a nucleic acid molecule selected from the group consisting of:

(a) a nucleic acid molecule comprising a sequence having at least 50% homology with the nucleic acid sequence of at least one of SEQ ID NOS. 1, 3, 5, 7 and 9 over a subsequence of at least 100 residues;

(b) a nucleic acid molecule which hybridizes under low, moderate or high stringency conditions with at least one of (i) the nucleic acid sequences of SEQ ID NOS. 1, 3, 5, 7 and 9, (ii) a complementary strand of a nucleic acid sequence of at least one of SEQ ID NOS. 1, 3, 5, 7 and 9, and a subsequence thereof of at least 100 nucleotides;

(c) a subsequence of (a) or (b), wherein the subsequence encodes a polypeptide, which can self-assemble to form a polymer; and

(d) a nucleic acid molecule that encodes a polypeptide having an amino acid sequence that has at least 50% identity with at least one amino acid sequence of SEQ ID NOS. 1, 3, 5, 7 and 9, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection.

101. (Amended) A computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a sequence of a nucleic acid molecule selected from the group consisting of:

(a) a nucleic acid molecule comprising a sequence having at least 50% homology with the nucleic acid sequence of at least one of SEQ ID NOS. 1, 3, 5, 7 and 9 over a subsequence of at least 100 residues;

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(b) a nucleic acid molecule which hybridizes under low, moderate or high stringency conditions with at least one of (i) the nucleic acid sequences of SEQ ID NOS. 1, 3, 5, 7 and 9, (ii) a complementary strand of a nucleic acid sequence of at least one of SEQ ID NOS. 1, 3, 5, 7 and 9, and a subsequence thereof of at least 100 nucleotides;

(c) a subsequence of (a) or (b), wherein the subsequence encodes a polypeptide, which can self-assemble to form a polymer; and

(d) a nucleic acid molecule that encodes a polypeptide having an amino acid sequence that has at least 50% identity with at least one amino acid sequence of SEQ ID NOS. 1, 3, 5, 7 and 9, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection.

105. (Amended) A method for comparing a first sequence to a second sequence comprising the steps of:

reading the first sequence and the second sequence through use of a computer program which compares sequences; and

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determining differences between the first sequence and the second sequence with the computer program, wherein said first sequence is a sequence of a nucleic acid molecule selected from the group consisting of:

(a) a nucleic acid molecule having a sequence having at least 50% homology with the nucleic acid sequence of at least one of SEQ ID NOS. 1, 3, 5, 7 and 9 over a subsequence of at least 100 residues;

(b) a nucleic acid molecule which hybridizes under low, moderate or high stringency conditions with at least one of (i) the nucleic acid sequences of SEQ ID NOS. 1, 3, 5, 7 and 9, (ii) a complementary strand of a nucleic acid sequence of at least one of SEQ ID NOS. 1, 3, 5, 7 and 9, and a subsequence thereof of at least 100 nucleotides;

(c) a subsequence of (a) or (b), wherein the subsequence encodes a polypeptide, which can self-assemble to form a polymer; and

#11 (d) a nucleic acid molecule that encodes a polypeptide having an amino acid sequence that has at least 50% identity with at least one amino acid sequence of SEQ ID NOS. 1, 3, 5, 7 and 9, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection.

107. (Amended) A method for identifying a feature in a particular sequence comprising the steps of:

reading the particular sequence using a computer program which identifies one or more features in a sequence; and

identifying one or more features in the particular sequence with the computer program, wherein the particular sequence is a sequence of a nucleic acid molecule selected from the group consisting of:

#12 (a) a nucleic acid molecule comprising a sequence having at least 50% homology with the nucleic acid sequence of at least one of SEQ ID NOS. 1, 3, 5, 7 and 9 over a subsequence of at least 100 residues;

(b) a nucleic acid molecule which hybridizes under low, moderate or high stringency conditions with at least one of (i) the nucleic acid sequences of SEQ ID NOS. 1, 3, 5, 7 and 9, (ii) a complementary strand of a nucleic acid sequence of at least one of SEQ ID NOS. 1, 3, 5, 7 and 9, and a subsequence thereof of at least 100 nucleotides;

(c) a subsequence of (a) or (b), wherein the subsequence encodes a polypeptide, which can self-assemble to form a polymer; and

(d) a nucleic acid molecule that encodes a polypeptide having an amino acid sequence that has at least 50% identity with at least one amino acid sequence of SEQ ID NOS. 1, 3, 5, 7 and 9, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection.

108. (Amended) A protein preparation comprising a polypeptide having an amino acid sequence selected from the group consisting of:

(a) an amino acid sequence selected from SEQ ID NOS. 2, 4, 6, 8 and10;

(b) an amino acid sequence selected from the group consisting of SEQ ID NOS. 2, 4, 6, 8 and 10, wherein the amino acid sequence has at least one conservative substitution; wherein the polypeptide comprising the amino acid sequence (b) can self-assemble to form a polymer; and

(c) an amino acid sequence comprising a fragment of at least one amino acid residue of SEQ ID NOS. 2, 4, 6, 8 and 10, wherein the polypeptide comprising the amino acid sequence (c) can self-assemble to form a polymer.

109. (Amended) An expression vector capable of replicating in a host cell comprising a polynucleotide having a sequence of a nucleic acid molecule selected from the group consisting of:

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(a) a nucleic acid molecule comprising a sequence having at least 50% homology with the nucleic acid sequence of at least one of SEQ ID NOS. 1, 3, 5, 7 and 9 over a subsequence of at least 100 residues;

(b) a nucleic acid molecule which hybridizes under low, moderate or high stringency conditions with at least one of (i) the nucleic acid sequences of SEQ ID NOS. 1, 3, 5, 7 and 9, (ii) a complementary strand of a nucleic acid sequence of at least one of SEQ ID NOS. 1, 3, 5, 7 and 9, and a subsequence thereof of at least 100 nucleotides;

(c) a subsequence of (a) or (b), wherein the subsequence encodes a polypeptide, which can self-assemble to form a polymer; and

(d) a nucleic acid molecule that encodes a polypeptide having an amino acid sequence that has at least 50% identity with at least one amino acid sequence of SEQ ID NOS. 1, 3, 5, 7 and 9, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection.

Please add new claims113-131 as set forth below:

--113. (New) A host cell as claimed in claim 109, wherein the host is selected from the group consisting of prokaryotes, eukaryotes, funguses, yeasts, plants and metabolically rich hosts.

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114. (New) The method as claimed in claim 34, wherein the vector is selected from the group consisting of viral vectors, plasmid vectors, phage vectors, phagemid vectors, cosmids, fosmids, bacteriophages, artificial chromosomes, adenovirus vectors, retroviral vectors, and adeno-associated viral vectors.

115. (New) The method as claimed in claim 34, wherein the host is selected from the group consisting of prokaryotes, eukaryotes, funguses, yeasts, plants and metabolically rich hosts.

116. (New) The method as claimed in claim 45, wherein the step of modifying said sequence by one or more steps selected from the group consisting of modifying one or more nucleotides in said sequence to another non-natural nucleotide, deleting one or more nucleotides in said sequence, and adding one or more non-natural nucleotides to said sequence.

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117. (New) The method as claimed in claim 46, wherein the step of modifying said sequence is repeated.

118. (New) The method as claimed in claim 47, wherein the step of modifying said sequence is repeated.

119. (New) The method as claimed in claim 48, wherein the step of modifying said sequence is repeated.

120. (New) The method as claimed in claim 49, wherein the step of modifying said sequence is repeated.

121. (New) The method as claimed in claim 50, wherein the step of modifying said sequence is repeated.

122. (New) The method as claimed in claim 51, wherein the step of modifying said sequence is repeated.

123. (New) The method as claimed in claim 52, wherein the step of modifying said sequence is repeated.

124. (New) The method as claimed in claim 53, wherein the step of modifying said sequence is repeated.

125. (New) The method as claimed in claim 54, wherein the step of modifying said sequence is repeated.

126. (New) The method as claimed in claim 55, wherein the step of modifying said sequence is repeated.

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127. (New) The method as claimed in claim 56, wherein the step of modifying said sequence is repeated.

128. (New) The method as claimed in claim 57, wherein the step of modifying said sequence is repeated.

129. (New) The method as claimed in claim 58, wherein the step of modifying said sequence is repeated.

130. (New) The method as claimed in claim 59, wherein the step of modifying said sequence is repeated.

131. (New) The method as claimed in claim 116, wherein the step of modifying said sequence is repeated.